

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 28, 2004, 17:42:42 ; Search time 1382.53 Seconds
(without alignments)
9232.292 Million cell updates/sec

Title: US-09-490-609b-280
Perfect score: 312
Sequence: 1 tcacaccagctgtgcatg.....aggctcatgtgcacacatg 312

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: GenBml:*
2: gb_ba:*
3: gb_htg:*
4: gb_in:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_ph:*
23: em_pl:*
24: em_pl:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_un:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	299.4	96.0	1605	AB037934	AB037934 Rattus no
2	298.4	95.6	1594	10 R43CAP1	D38467 Rat mRNA fo
3	293.4	94.0	1594	10 R43CAP1	X69021 R.norvegicu
4	285.4	91.5	1216	6 E09237	E09237 cDNA insert
5	216.8	69.5	1598	6 BC012710	BC012710 Mus muscu
6	214.8	68.8	1573	6 BD168858	BD168858 Senescenc
7	214.8	68.8	1573	6 NMU28937	U28937 Mus musculu
8	190	60.9	1109	10 D67071S2	D67071 Mus musculu
9	184.2	59.0	400	2 AC115307	D67068 Rat gene fo
10	184.2	59.0	260600	2 AC115307	AC115307 Rattus no
11	170.4	54.6	1375	9 AB028125	AB028125 Homo sapi
12	168.8	54.1	1356	6 AX409001	AX409001 Sequence
13	168.8	54.1	1356	6 BD079930	BD079930 Cancer-as
14	168.8	54.1	1356	6 E09013	E09013 cDNA encodi
15	168.8	54.1	1356	9 HUMSMP30	D31815 Human mRNA
16	168	53.8	1394	4 AB035446	AB035446 Bos tauru
17	160	51.3	1131	4 AB110216	AB110216 Mesocrici
18	147.4	47.2	216812	10 AL672073	AL672073 Mouse sap
19	146.6	47.0	1438	9 AB032064	AB032064 Homo sapi
20	145.8	46.7	2280	10 MMU32170	U32170 Mus musculu
21	127	40.7	1357	4 AB035445	AB035445 Oryctolag
22	113	36.2	145456	9 AL513366	AL513366 Human DNA
23	97.6	31.3	1126	5 AB037936	AB037936 Xenopus 1
24	96	30.8	1088	5 AB033368	AB033368 Xenopus 1
25	95.2	30.5	1221	5 AB037935	AB037935 Gallus ga
26	77	24.7	867	10 D67071S1	D67071 Rat gene fo
27	57.4	18.4	142125	2 AC129835	AC129835 Canis fam
28	46.8	15.0	441	10 D67071S3	D67070 Rat gene fo
29	41	13.1	236629	9 AC120586	AC120586 Rattus no
30	41	13.1	280710	2 AC105612	AC105612 Rattus no
31	40.6	13.0	162509	2 AL137852	AL137852 Human DNA
32	39.6	12.7	36933	9 AC107074	AC107074 Homo sapi
33	38.4	12.3	176710	2 AC129434	AC129434 Rattus no
34	38.4	12.3	246362	2 AC111797	AC111797 Rattus no
35	37.2	11.9	229561	2 AC120067	AC120067 Rattus no
36	37	11.9	105087	9 AC093884	AC093884 Homo sapi
37	37	11.9	160196	2 AC016701	AC016701 Homo sapi
38	36.8	11.8	66619	2 AC100648	AC100648 Mus muscu
39	36.8	11.8	179705	10 AL627087	AL627087 Mouse DNA
40	36.8	11.8	181623	9 AL158071	AL158071 Human DNA
41	36.6	11.7	100562	9 AL355870	AL355870 Human DNA
42	36.4	11.7	153645	9 AC025426	AC025426 Homo sapi
43	36.4	11.7	175181	2 AC110529	AC110529 Mus muscu
44	36.4	11.7	183416	10 AL671269	AL671269 Mouse DNA
45	36.4	11.7	208700	2 AC140319	AC140319 Mus muscu

ALIGNMENTS

RESULT 1	AB037934	1605 bp	mRNA	linear	ROD 09-FEB-2000
LOCUS	AB037934				
DEFINITION	Rattus norvegicus mRNA for regucalcin, complete cds.				
ACCESSION	AB037934				
VERSION	AB037934.1	GI:6970312			
KEYWORDS	regucalcin.				
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Rattus norvegicus				
REFERENCE	1 (sites)				
AUTHORS	Misawa, H. and Yamaguchi, M.				
TITLE	The gene family encoding the calcium-binding protein regucalcin				

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1605)
AUTHORS Yamaguchi, M. and Misawa, H.
TITLE Direct Submission
JOURNAL Submitted (02-FEB-2000) Masayoshi Yamaguchi, Graduate School of
Nutritional Sciences, University of Shizuoka, Laboratory of
Endocrinology and Molecular Metabolism, 52-1 Yada, Shizuoka
422-8526, Japan (E-mail: yamaguchifnsl.u-shizuoka-ken.ac.jp,
Tel: +81-54-264-5580, Fax: +81-54-264-5580)

FEATURES
source location/Qualifiers
1..1605
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/cell_line="H4-II-E"
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99..398
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/product="regucalcin"
/protein_id="BAA90692.1"
/db_xref="GI:6970313"
/translation="MSISIKIECVLRNRYRCSPPWEBSKCLLPVDIPSKTVCRWDS
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DHRIFYIDLSYTVDAFDYDLPDQIISNRIVYKMEKDEQIPDMCIDVEGKLWAC
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CDS

BASE COUNT 471 a 300 c 367 g 467 t
ORIGIN

Query Match 96.0%; Score 299.4; DB 10; Length 1605;
Best Local Similarity 99.4%; Pred. No. 2.9e-77;
Matches 311; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 TTCAACCCAGGTGTGATCTGAGTGTCTCTTGTCTTCAATTTAAAGATATCTTG 60
DB 6 TTCAACCCAGGTGTGATCTGAGTGTCTCTTGTCTTCAATTTAAAGATATCTTG 65
QY 61 AAAAAACCTGTACGTCTCTTCTCGGACCATGCTTCATCAAGATTGAATGTT 120
DB 66 AAAAAACCTGTACGTCTCTTCTCGGACCATGCTTCATCAAGATTGAATGTT 125
QY 121 TTAAGGAGAACTACAGGTGTGGAGTCCCTGTGTGGAGAGGAGCATCAAGTGTCTG 180
DB 126 TTAAGGAGAACTACAGGTGTGGAGTCCCTGTGTGGAGAGGAGCATCAAGTGTCTG 185
QY 181 CTGTGTGTAGACATCCCTTCAAGACTGTCTGCCGATGGATTGATCAGCAATCGAGTG 240
DB 186 CTGTGTGTAGACATCCCTTCAAGACTGTCTGCCGATGGATTGATCAGCAATCGAGTG 245
QY 241 CACGAGTTGGTGTAGATGCCCAAGTCAGTTCAGTGGCA-TTGCAGAGTCAGAGGCTAT 299
DB 246 CACGAGTTGGTGTAGATGCCCAAGTCAGTTCAGTGGCACTTGACAGTGAAGGCTAT 305
QY 300 GTTGCCACCATGG 312
DB 306 GTTGCCACCATGG 318
RESULT 2
RATCBP1 1594 bp mRNA linear ROD 08-FEB-1999
LOCUS Rat mRNA for calcium-binding protein, complete cds.
ACCESSION D38467.1 GI:600378
VERSION D38467.1 GI:600378
KEYWORDS calcium-binding protein; regucalcin.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases)
AUTHORS Shimokawa, N. and Yamaguchi, M.

TITLE Molecular cloning and sequencing of the cDNA coding for a
calcium-binding protein regucalcin from rat liver
JOURNAL FEBS Lett. 327 (3), 251-255 (1993)
MEDLINE 93351639
PUBMED 8348951
REFERENCE 2 (bases 1 to 1594)
AUTHORS Shimokawa, N. and Yamaguchi, M.
JOURNAL Unpublished
COMMENT On Dec 8, 1994 this sequence version replaced gi:391851.
D16386:Submitted(07-Jun-1993) to DDBJ by:Masayoshi Yamaguchi
Submitted (03-OCT-1994) to DDBJ by:
Masayoshi Yamaguchi
Graduate School of Nutritional Sciences
University of Shizuoka
52-1 Yada
Shizuoka 422.

FEATURES

source location/Qualifiers
1..1594
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Wistar"
/db_xref="taxon:10116"
/tissue_type="liver"
93..992
/codon_start=1
/product="regucalcin"
/protein_id="BAA07490.1"
/db_xref="GI:408807"
/translation="MSISIKIECVLRNRYRCSPPWEBSKCLLPVDIPSKTVCRWDS
ISNRVQRVGVDAVSSVALRQSGYVATIGTRCALNEDQSFLLAMDEKKNRP
NDKRVDPAGRYFAGTMAETAPAVLERHQSLSPDPHSVKYFPQVVISGLDWSL
DHRIFYIDLSYTVDAFDYDLPDQIISNRIVYKMEKDEQIPDMCIDVEGKLWAC
YNGGAVIRLDPETGRLOTVKLPVDKTSRCCFGKDYSEMYVTCARDGMSAEGLLRQF
DAGNIFKITGLGVKGIAPYSYAG"

CDS

BASE COUNT 464 a 300 c 365 g 465 t
ORIGIN

Query Match 95.6%; Score 298.4; DB 10; Length 1594;
Best Local Similarity 99.4%; Pred. No. 5.7e-77;
Matches 310; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 TCAACCCAGGTGTGATCTGAGTGTCTCTTGTCTTCAATTTAAAGATATCTTGA 61
DB 1 TCAACCCAGGTGTGATCTGAGTGTCTCTTGTCTTCAATTTAAAGATATCTTGA 60
QY 62 AAAAAACCTGTACGTCTCTTCTCGGACCATGCTTCATCAAGATTGAATGTT 121
DB 61 AAAAAACCTGTACGTCTCTTCTCGGACCATGCTTCATCAAGATTGAATGTT 120
QY 122 TTAAGGAGAACTACAGGTGTGGAGTCCCTGTGTGGAGAGGAGCATCAAGTGTCTGC 181
DB 121 TTAAGGAGAACTACAGGTGTGGAGTCCCTGTGTGGAGAGGAGCATCAAGTGTCTGC 180
QY 182 TGTGTGTAGACATCCCTTCAAGACTGTCTGCCGATGGATTGATCAGCAATCGAGTGC 241
DB 181 TGTGTGTAGACATCCCTTCAAGACTGTCTGCCGATGGATTGATCAGCAATCGAGTGC 240
QY 242 AGCGAGTTGGTGTAGATGCCCAAGTCAGTTCAGTGGCA-TTGCAGAGTCAGAGGCTATG 300
DB 241 AGCGAGTTGGTGTAGATGCCCAAGTCAGTTCAGTGGCACTTGACAGTGAAGGCTATG 300
QY 301 TTGCCACCATGG 312
DB 301 TTGCCACCATGG 312
RESULT 3
RNSMP30A 1594 bp mRNA linear ROD 16-NOV-1993
LOCUS RNSMP30A
DEFINITION R.norvegicus SMP30 mRNA for senescence marker protein-30.
ACCESSION X69021.1 GI:57254
VERSION X69021.1 GI:57254

KEYWORDS senescence marker protein-30.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1594)
AUTHORS Fujita,T., Shiraawa,T., Uchida,K. and Maruyama,N.
TITLE Isolation of cDNA clone encoding rat senescence marker protein-30
(Smp30) and its tissue distribution
JOURNAL Biochim. Biophys. Acta 1132 (3), 297-305 (1992)
MEDLINE 93041931
PUBMED 1420310
REFERENCE 2 (bases 1 to 1594)
AUTHORS Fujita,T.
TITLE Direct Submision
JOURNAL Submitted (08-DEC-1992) T. Fujita, Dept. o Molecular Biology, Tokyo
Metropolitan Inst. of Gerontology, 35-2, Sakaecho, Itabashi-Ku,
Tokyo 173, JAPAN
FEATURES
source Location/Qualifiers
1..1594
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Wistar/Sic"
/db_xref="taxon:10116"
/dev_stage="6 months"
88..1588
/gene="SMP30"
88..987
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/codon_start=1
/product="senescence marker protein-30"
/protein_id="CAA48786.1"
/db_xref="GI:57255"
/db_xref="SWISS-PROT:Q03336"
/translation="MSSIKIEVLRNRCGSPWEASKLLFVDIPSKTCVRMS
ISNRVGVADAVSSVALRSGVYATIGTKCALNWDOSVFILAMVDEBKNNRF
NIDKVDPAAGYFAGTAAEPALVLERRGSLSLPPDSVKKYFPQVVISGLDWSL
DHKIFVYDLSLSTVDAFDYDLPDGOISNRRTYVKMEKDOI PDGWCIDVEGLWAC
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polya_site 1588
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Best Local Similarity 99.3%; Pred. No. 1.7e-75;
Matches 305; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 7 CCCAGGTGAGTGTGAGTGTCTTCTTGTCTTCAATTTAAAGATATCTGAAAAA 66
Db 1 CCAGGTGTGAGTGTGAGTGTCTTCTTGTCTTCAATTTAAAGATATCTGAAAAA 60
QY 67 ACCTGTACTGTCTTCTTCTGCGACCATGTCTTCATCAAGATTGAATGTTTAAAG 126
Db 61 ACCTGTACTGTCTTCTTCTGCGACCATGTCTTCATCAAGATTGAATGTTTAAAG 120
QY 127 GAAACATCAGGTGTGGGAGTCCCTGTGTGGAGAGGACATCAAGTGTCTGCTTT 186
Db 121 GAAACATCAGGTGTGGGAGTCCCTGTGTGGAGAGGACATCAAGTGTCTGCTTT 180
QY 187 GTAGACATCCCTTCAAGACTGTCTGCGATGGGATTCGATCAGCAATCAGTGCAGCGA 246
Db 181 GTAGACATCCCTTCAAGACTGTCTGCGATGGGATTCGATCAGCAATCAGTGCAGCGA 240
QY 247 GTTGTGTGAATGCCCATGTCAGTTCAGTGGCA-TTCGACAGTCAGAGGCTATGTTGCC 305
Db 241 GTTGTGTGAATGCCCATGTCAGTTCAGTGGCA-TTCGACAGTCAGAGGCTATGTTGCC 300

QY 306 ACCATCG 312
Db 301 ACCATTG 307
RESULT 4
LOCUS E09237 1216 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA insert encoding Regucalcin.
ACCESSION E09237
VERSION E09237.1 GI:22025863
KEYWORDS JP 1995123985-A/1.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1216)
AUTHORS Yamaguchi,M.
TITLE DNA FRAGMENT CODING FOR REGUCALCIN
JOURNAL Patent: JP 1995123985-A 1 16-MAY-1995;
YAMAGUCHI MASAYOSHI, DAI ICHI PURE CHEM CO LTD
COMMENT OS Rattus sp. (Rat)
PN JP 1995123985-A/1
PD 16-MAY-1995
PF 09-NOV-1993 JP 1993279349
PI YAMAGUCHI MASAYOSHI
PC C12N15/09,C12N1/21,C12N1/21,C12R1.19;
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH source 1..1216
FT /organism="Rattus sp."
FT /mol_type="genomic RNA"
FT /db_xref="taxon:10118"
BASE COUNT 338 a 231 c 309 g 338 t
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Best Local Similarity 99.3%; Pred. No. 3.8e-73;
Matches 297; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 15 TGAATCTGAGTGTCTTCTTGTCTTCAATTTAAAGATATCTGAAAAAACCTGTCA 74
Db 1 TGAATCTGAGTGTCTTCTTGTCTTCAATTTAAAGATATCTGAAAAAACCTGTCA 60
QY 75 CTGTCTTTTCTGCGACCATGTCTTCATCAAGATTGAATGTTTAAAGGAGAACTA 134
Db 61 CTGTCTTTTCTGCGACCATGTCTTCATCAAGATTGAATGTTTAAAGGAGAACTA 120
QY 135 CAGGTGTGGGAGTCCCTGTGTGGAGAGGACATCAAGTGTCTGCTTTGTAGACT 194
Db 121 CAGGTGTGGGAGTCCCTGTGTGGAGAGGACATCAAGTGTCTGCTTTGTAGACT 180
QY 195 CCGTTCAAGACTGTCTGCGATGGGATTCGATCAGCAATCAGTGCAGAGTGTGT 254
Db 181 CCGTTCAAGACTGTCTGCGATGGGATTCGATCAGCAATCAGTGCAGAGTGTGT 240
QY 255 AGATGCCCATCAGTTCAGTGGCA-TTCGACAGTCAGAGGCTATGTTGCCACCATG 312
Db 241 AGATGCCCATCAGTTCAGTGGCA-TTCGACAGTCAGAGGCTATGTTGCCACCATG 299
RESULT 5
LOCUS BC012710 1598 bp mRNA linear ROD 16-APR-2003

DEFINITION Mus musculus regucalcin, mRNA (cDNA clone MGC:14006 IMAGE:4210374), complete cds.

ACCESSION BC012710

VERSION BC012710.1 GI:15215230

KEYWORDS MGC

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 1598)

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Krausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max A.S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Staptchuk M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetzl T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez J., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schultz J., Myers R.M., Bicksteadt Y.S., Krzywinski M.I., Skalska U., Smalusz D.E., Schnerker A., Schein J.E., Jones S.J. and Marra M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 1598)

12477932

Strausberg R.

Direct Submission

Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

REMARK COMMENT

Contact: MGC help desk

Email: cgaps-rc@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadansystemsbiology.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.lnl.gov>

Series: IRAX Plate: 18 Row: n Column: 22

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6677738.

FEATURES

source

1.1598

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/strain="FVB/N"

/db_xref="taxon:10090"

/clone="MGC:14006 IMAGE:4210374"

/tissue_type="liver, normal, 5 month old male mouse."

/clone_lib="NCI_CGAP_L19"

/lab_host="DHI10B"

/note="Vector: pCMV-SPORT6"

1.1598

/gene="Rgn"

/note="synonym: SMP30"

/db_xref="LocusID:19733"

/db_xref="MGI:108024"

gene

CDS

86..985

/codon_start=1

/product="regucalcin"

/protein_id="AAH12710.1"

/db_xref="GI:15215231"

/db_xref="LocusID:19733"

/translation="MSSIKRECVLRNENRRCESPVWEASQSLFVDPISKIKCMTDVSNOYORAVADPVSSVALRQGGVATIGTKFCALNMENOSVFLAVDEKKNRFNDGKDPAGRGFAGTMAETAPAVLERRHQSLYSLEPDSVYKVEPDVDISGLDMSLDKIFVYIDSLSYTADAPYDLOTQOISNRRIYKMEDEQIPDMCIDAEGLWVACVAGGVIRLDPEPTGRRLQTKLPVKRTSSCCGSDYSBMYTCARDGLNAGLLRQPDAGNFKITGLGVKRIAPSYNG"

BASE COUNT 466 a 293 c 370 g 469 t

ORIGIN

Query Match 69.5%; Score 216.8; DB 10; Length 1598;

Best Local Similarity 88.1%; Pred. No. 6.6e-53;

Matches 259; Conservative 0; Mismatches 32; Indels 3; Gaps 2;

QY 22 TGGAGTGTTCCTTTGCTCTCTATTATTTAAAGATATCTGAAAAAACCCTG--TCACTGTC 79

DB 12 TGGAGTGTTCCTTTGCTCTCTATTATTTAAAGATATCTGAAAAAACCCTGACTGTC 71

QY 80 CTTTTCCTGCGACATGCTCTTCCATCAAGATTGAATGCTTTTAAGGAGAACTACAGGT 139

DB 72 CTTTTCCTGCGACATGCTCTTCCATCAAGATTGAATGCTTTTAAGGAGAACTACAGGT 131

QY 140 GTGGGAGTCCCTGCTGTGAGGAGGAGCATCAAGTGTCTGTTTGTAGACATCCCTT 199

DB 132 GTGGGAGTCTCTCTGTATGAGGAGGAGGAGTCAAGTGTCTGTTTGTAGATCCCTT 191

QY 200 CAAAGACTGTCTGCTGAGTGGATTCGATCGAATCGAATCGAGTGGTGTAGATG 259

DB 192 CAAAGATTTTGTGATGAGTACGATCGATCAAGTCAAGTCAAGTGTGTGAGATG 251

QY 260 CCCCAGTCACTTCAGTGGCA--TTGACAGTCAAGGAGGCTATGTTGCCACCATGG 312

DB 252 CCCCAGTCACTTCAGTGGCACTTGCACAGTGGAGGCTATGTTGCCACCATGG 305

RESULT 6

BD168858 1573 bp DNA linear PAT 17-JAN-2003

LOCUS

DEFINITION BD168858 Senseence marker protein 30-deficient non-human animal, antibody and method of constructing the same.

ACCESSION BD168858

VERSION BD168858.1 GI:27874670

KEYWORDS WO 0234041-A/1.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 1573)

Maruyama N. and Kasahara Y.

Senseence marker protein 30-deficient non-human animal, antibody and method of constructing the same

Patent: WO 0234041-A 1 02-MAY-2002;

NAOKI MARUYAMA, YASUSHI KASAHARA

JOURNAL

OS Mus musculus (mouse)

PN WO 0234041-A/1

PD 02-MAY-2002

PF 22-OCT-2001 WO 2001JP009243

PR 23-OCT-2000 JP 00P 322234

PI NAOKI MARUYAMA, YASUSHI KASAHARA

PC A01K67/027, C12N15/12, C07K14/47, C12P21/08, C12N15/06 CC

Senseence marker protein 30-deficient non-human animal, CC antibody and

CC method of constructing the same

FH Key Location/Qualifiers

FT source 1.1573

FEATURES

source

1.1573

Location/Qualifiers

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BASE COUNT 305 a 207 c 282 g 315 t

ORIGIN

Query Match 60.9%; Score 190; DB 10; Length 1109;
 Best Local Similarity 89.3%; Pred. No. 5.3e-45;
 Matches 216; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

QY 72 TCACGTGCTTTCCCTGCGACCATGCTTCATCAAGATGAANGTTTAAAGGAGAA 131
 DB 3 TCACGTGCTTTCCCTGCGACCATGCTTCATCAAGATGAANGTTTAAAGGAGAA 62
 QY 132 CTACAGGTGGGAGAGTCCCTGTGTGGAGAGGAGCATCAAGTGTCTGTTTGTAGA 191
 DB 63 CTACAGGTGGGAGAGTCCCTGTGTGGAGAGGAGCATCAAGTGTCTGTTTGTAGA 122
 QY 192 CATCCCTTCAAAGACTGTCTGCCGATGGATTGATAGCAATCGAGTCAGGAGTTGG 251
 DB 123 TATCCCTTCAAAGACTGTCTGCCGATGGATTGATAGCAATCGAGTCAGGAGTTGG 182
 QY 252 TGTAGATGCCCCAGTCAGTCAATGGCA-TTCCAGCAGTCAGAGGCTATGTCACCAT 310
 DB 183 TGTAGATGCCCCAGTCAGTCAATGGCA-TTCCAGCAGTCAGAGGCTATGTCACCAT 242
 QY 311 GG 312
 DB 243 TG 244

RESULT 9
 LOCUS D67071S2 400 bp DNA linear ROD 14-APR-2000
 DEFINITION Rat gene for regucalcin, exon2.
 ACCESSION D67069
 VERSION D67069.1 GI:1015329
 KEYWORDS regucalcin.
 SEGMENT 2 of 3
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE
 AUTHORS Yamaguchi, M., Makino, R. and Shimokawa, N.
 TITLE The 5' end sequences and exon organization in rat regucalcin gene
 JOURNAL Mol. Cell. Biochem. 165 (2), 145-150 (1996)
 MEDLINE 8979263
 PUBMED 2 (bases 1 to 400)
 REFERENCES Yamaguchi, M., Makino, R. and Shimokawa, N.
 AUTHORS Characterization of the 5' end sequences and exon organization in
 TITLE rat regucalcin gene
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 400)
 AUTHORS Yamaguchi, M.
 TITLE Direct Submission
 JOURNAL Submitted (27-SEP-1995) Masayoshi Yamaguchi, Graduate School of
 Nutritional Sciences, University of Shizuoka, Laboratory of
 Metabolism and Endocrinology; 52-1 Yada, Shizuoka, Shizuoka 422,
 Japan (Tel:054-264-5580, Fax:054-264-5580)
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 Matches 195; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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 QY 130 AACTACAGGTGGGAGAGTCCCTGTGTGGAGAGGAGCATCAAGTGTCTGTTTGTAGA 189
 DB 181 AACTACAGGTGGGAGAGTCCCTGTGTGGAGAGGAGCATCAAGTGTCTGTTTGTAGA 240
 QY 190 GACATCCCTTCAAAGACTGTCTGCCGATGGATTGATAGCAATCGAGTCAGGAGTT 249
 DB 241 GACATCCCTTCAAAGACTGTCTGCCGATGGATTGATAGCAATCGAGTCAGGAGTT 300
 QY 250 GGTGTAGATGCCCCAGTCAGTCAATGGCA-TTCCAGCAGTCAGAGGCTATGTCACCAT 282
 DB 301 GGTGTAGATGCCCCAGTCAGTCAATGGCA-TTCCAGCAGTCAGAGGCTATGTCACCAT 333

RESULT 10
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 DEFINITION Rattus norvegicus clone CH230-11F18, WORKING DRAFT SEQUENCE.
 ACCESSION AC115307
 VERSION AC115307.4 GI:24817861
 KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE
 AUTHORS Muzny, D., Marie, Metzger, M., Lee, A., Abramson, S., Adams, C., Alder, J.,
 Allen, C., Allen, H., Altschrocks, S., Amin, A., Anguiano, D.,
 Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
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Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 260600)
2 (bases 1 to 260600)
Worley, K.C.
Direct Submission
Submitted (17-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 260600)
Baylor College of Medicine
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2002 this sequence version replaced gi:22772493.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Project name: GEBE
Center project name: CH230-11F18
----- Summary Statistics
Assembly program: Phrap, version 0.990329
Consensus quality: 229014 bases at least Q40
Consensus quality: 231787 bases at least Q30
Consensus quality: 232904 bases at least Q20
Estimated insert size: 237320, sum-of-contigs estimation
Quality coverage: 7x in Q20 bases, sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_drafc_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have

FEATURES					
source					
		* Provided by the submittor.			
		* This sequence will be replaced			
		* by the finished sequence as soon as it is available and			
		* the accession number will be preserved.			
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Best Local Similarity	91.5%; Pred. No. 3e-43;				
Matches 195; Conservative	0; Mismatches 18; Indels 0; Gaps 0;				
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Oy	130 AACTACAGTGTTGGGAGATCCCCGTGTGTGGAGAGGCATCAAAGTGTCTGCTTTGTA 189				
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Dd	95082 GACATCCCTTCAAGAAGCTGTCTGCCATGGGATTGCATACGCAATGAGTGCAGCGAGTT 95144				
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Dd	95142 GGTTAGATGATTCAGTGGCATTCAGTGGCATTC 95174				
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LOCUS	AB028125				
DEFINITION	Homo sapiens mRNA for regucalcin, complete cds.				
ACCESSION	AB028125				
VERSION	AB028125.1 GI:5030903				
KEYWORDS	regucalcin.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
	1 (sites)				
	Misawa,H. and Yamaguchi,M.				
REFERENCE	Transcript heterogeneity of the human gene for Ca ²⁺ -binding protein				
AUTHORS	regucalcin				
TITLE	Int. J. Mol. Med. 5 (3), 283-287 (2000)				
JOURNAL	Medline				
PUBMED	20144201				
REFERENCES	10677570				
AUTHORS	2 (bases 1 to 1375)				
TITLE	Yamaguchi,M. and Misawa,H.				
JOURNAL	Direct Submission				
	Submitted (31-MAY-1999) Masayoshi Yamaguchi, Graduate School of				

Nutritional Sciences, University of Shizuoka, Laboratory of Endocrinology and Molecular Metabolism, Yada 52-1, Shizuoka 422-8526, Japan (E-mail: yamaguchi@mail.u-shizuoka-ken.ac.jp, Tel: +81-54-264-5580, Fax: +81-54-264-5580)

FEATURES

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CDS

BASE COUNT 392 a 274 c 343 g 366 t

ORIGIN

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Best Local Similarity 76.3%; Pred. No. 3.2e-39;
Matches 235; Conservative 0; Mismatches 71; Indels 2; Gaps 2;

QY 6 ACCAGGTGTGATGCTGGAGTGTTCCTTCTCTATTTAAAGATCTTGAAGAA 65
DB 8 ACCAAGAGAGGAGGTCGAGTGTCACTTTTGTCTTTTGAAGATCTTGAAG 67
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DB 68 AACACGTCACTGTATCTCC-CTCGACCATGTCTTCATTAAGATGATGTGTTGCC 126
QY 126 GGAGAACTACAGTGTGGGAGTCCCTGTGTGGAGAGCATCAAGTGTGCTGT 185
DB 127 AGAAGACTGCGGAGTGTGAGTCTCAGATGGAGAGATGCCAATCTCTGCTCT 186
QY 186 TGTAGACATCTCTTCAAGACTGTCTGCCATGGATTCATCAGCAATGATGACG 245
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DB 307 CACCATGG 314

RESULT 12
AX409001 1356 bp DNA linear PAT 14-JUN-2002

LOCUS AX409001
DEFINITION Sequence 1648 from Patent WO0229103.
ACCESSION AX409001
VERSION AX409001.1 GI:21441706

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Alvarez, C., Horne, D., Peres-da-Silva, S. and Vockley, J. G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 1648 11-Apr-2002;
GENE LOGIC INC (US)

FEATURES
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Best Local Similarity 76.0%; Pred. No. 9.4e-39;
Matches 234; Conservative 0; Mismatches 72; Indels 2; Gaps 2;

QY 6 ACCAGGTGTGATGCTGGAGTGTTCCTTCTCTATTTAAAGATCTTGAAGAA 65
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QY 126 GGAGAACTACAGTGTGGGAGTCCCTGTGTGGAGAGCATCAAGTGTCTGTGT 185
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DB 306 CACCATGG 313

RESULT 13
BD079930 1356 bp DNA linear PAT 27-AUG-2002

LOCUS BD079930
DEFINITION Cancer-associated nucleic acids and polypeptides.
ACCESSION BD079930
VERSION BD079930.1 GI:22625533

KEYWORDS JP 2001516009-A/596.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Old, L. J., Scarnlan, M. J., Stockert, F., Gure, A., Chen, Y. T., Gout, I.,
Oghare, M., Obata, Y., Pfundschuh, M., Tureci, O. and Sahin, U.
TITLE Cancer-associated nucleic acids and polypeptides
JOURNAL Patent: JP 2001516009-A 596 25-SEP-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH

OS Homo sapiens (human)
PN JP 2001516009-A/596
PD 25-SEP-2001
PR 15-JUL-1998 JP 2000503425
PR 17-JUL-1997 US 08/896164, 10-OCT-1997 US 60/061599 PR
10-OCT-1997 US 60/061765, 10-OCT-1997 US 08/948705 PR
11-OCT-1997 GB 9721697.2, 22-JUN-1998 US 09/102322 PI
J OLD, MATTHEW J SCARNLAN, ELISABETH STOCKERT, ALI GURE, YAO PI
CHEN, IVAN GOUT, MICHAEL O'HARE, YUICHI OBATA, MICHAEL PFUNDSCHECH, PI
OZLEM TURECI,
PI UGUR SAHIN

GOIN33/574, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00, PC
A61P35/00,
PC C07K14/82, C07K16/32, C12N15/09//C07K16/46, C12P21/08, A61K37/02,
PC C12N18/00
CC Cancer-associated nucleic acids and polypeptides. FH Key
Location/Qualifiers
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FT source
FT Location/Qualifiers

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BASE COUNT 373 a 274 c 343 g 366 t
 ORIGIN

Query Match 54.1%; Score 168.8; DB 6; Length 1356;
 Best Local Similarity 76.0%; Pred. No. 9.4e-39;
 Matches 234; Conservative 0; Mismatches 72; Indels 2; Gaps 2;

QY 6 ACCCAGGTGAGTGTGAGTGTTCCTTTGCTTCTATTTTAAAGATATCTGAAAA 65
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RESULT 14
 LOCUS E09013 1356 bp RNA linear PAT 29-SEP-1997
 DEFINITION CDNA encoding human-SMP30 protein.
 ACCESSION E09013
 VERSION E09013.1 GI:22025639
 KEYWORDS JP 1995097399-A/1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 1356)
 Fujita,K. and Maruyama,N.
 NEW POLYPEPTIDE AND REAGENT FOR MEASURING HUMAN SENSENCE MARKER
 PROTEIN SMP 30
 Patent: JP 1995097399-A 1 11-APR-1995;
 FUJIREBIO INC
 COMMENT OS Homo sapiens (Human)
 PN JP 1995097399-A/1
 PD 11-APR-1995
 PP 29-SEP-1993 JP 1993265681
 PT FUJITA KEIKO, MARUYAMA NAOKI
 PC C07K14/47,C12N15/09,C1201/68,G01N33/53,C07K99/00; CC
 strandedness: Double;
 CC topology: Linear;
 FH Key Location/Qualifiers
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 FT /tissue_type="hepatic"
 FT mat_peptide 94..990
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FEATURES
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 DEFINITION Human mRNA for SMP-30 (senescence marker protein-30), complete cds.
 ACCESSION D31815
 VERSION D31815.1 GI:1072311
 KEYWORDS SMP-30; senescence marker protein-30.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 1356)
 Fujita,T., Mandel,J.L., Shirasawa,T., Hino,O., Shirai,T. and
 Maruyama,N.
 Isolation of cDNA clone encoding human homologue of senescence
 marker protein-30 (SMP30) and its location on the X chromosome
 Biochim. Biophys. Acta 1263 (3), 249-252 (1995)
 JOURNAL MEDLINE
 PUBMED 7548213
 REFERENCE 2 (bases 1 to 1356)
 SHIRASAWA,T.
 Direct Submision
 Submitted (11-JUN-1994) Takuji Shirasawa, Tokyo Metropolitan
 Institute of Gerontology, Molecular Pathology, 35-2 Sakae-cho,
 Itabashi-ku, Tokyo 173, JAPAN (Tel:813-3964-3241 (ex.3034),
 Fax:813-3579-4776)
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QY	126	GGAGAACTAAGGTGTGGGAGTCCCTGTGTGGGAGAGGCATCAAAGTGTCTGCTGT	185
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